

WHAT IS CLAIMED IS:

1 1. A substantially pure peptide which is capable
2 of binding a PTB domain, wherein the peptide is from 5 to 100
3 amino acids in length, and comprises a core sequence of amino
4 acids $NX_3X_1X_2X_4$;

5 wherein X_1 is selected from the group consisting of
6 Y, pY or an analog thereof, E, T, D, Q, A and F;

7 X_2 is selected from pY or an analog thereof, and Y,
8 provided that at least one of X_1 and X_2 is pY, or an analog
9 thereof;

10 X_3 is selected from the group consisting of L and A;
11 and

12 X_4 is selected from the group consisting of W, L, S,
13 F and Q.

1 2. The peptide as recited in claim 1, wherein the
2 peptide is from 6 to 100 amino acids in length, and comprises
3 a core sequence of amino acids $X_5NX_3X_1X_2X_4$, wherein X_5 is
4 selected from the group consisting of D, S, E and A.

1 3. The peptide as recited in claim 2, wherein X_2
2 is pY.

1 4. The peptide as recited in claim 3, wherein the
2 peptide is from 6 to 100 amino acids in length, and comprises
3 a core sequence of amino acids selected from the group
4 consisting of $DNX_3X_1pYX_4$ and $ENX_3X_1pYX_4$, where X_4 is selected
5 from the group consisting of W and F.

1 5. The peptide as recited in claim 2, wherein the
2 peptide is from 12 to 100 amino acids in length, and comprises
3 a core sequence of amino acids selected from the group
4 consisting of AFDNLY(pY)WDQNS, AFDNL(pY)YWDQNS and
5 AFDNL(pY)(pY)WDQNS.

1 6. The peptide as recited in claim 2, wherein the
2 peptide is from 21 to 100 amino acids in length, and comprises

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3 a core sequence of amino acids selected from the group
 4 consisting of: PAFSPAFDNLY(pY)WDQNSSEQG;
 5 PAFSPAFDNL(pY)YWDQNSSEQG; PAFSPAFDNL(pY)(pY)WDQNSSEQG;
 6 PAFSPAADNLY(pY)WDQNSSEQG; PAFSPAADNL(pY)YWDQNSSEQG;
 7 PAFSPAADNL(pY)(pY)WDQNSSEQG; PAFSPAANLY(pY)WDQNSSEQG;
 8 PAFSPAANL(pY)YWDQNSSEQG; PAFSPAANL(pY)(pY)WDQNSSEQG;
 9 PAFSPAFLNLY(pY)WDQNSSEQG; PAFSPAFLNL(pY)YWDQNSSEQG;
 10 PAFSPAFLNL(pY)(pY)WDQNSSEQG; PAFSPAFDNAY(pY)WDQNSSEQG;
 11 PAFSPAFDNA(pY)YWDQNSSEQG; PAFSPAFDNA(pY)(pY)WDQNSSEQG;
 12 PAFSPAFDNLA(pY)WDQNSSEQG; PAFSPAFDNLF(pY)WDQNSSEQG;
 13 PAFSPAFDNLY(pY)FDQNSSEQG; PAFSPAFDNL(pY)YFDQNSSEQG;
 14 PAFSPAFDNL(pY)(pY)FDQNSSEQG; PAFSPAFDNLY(pY)WAQNSSEQG;
 15 PAFSPAFDNL(pY)YWAQNSSEQG; PAFSPAFDNL(pY)(pY)WAQNSSEQG;
 16 PAFSPAFDNLY(pY)WDANSSEQG; PAFSPAFDNL(pY)YWDANSSEQG;
 17 PAFSPAFDNL(pY)(pY)WDANSSEQG; PAFSPAFDNLY(pY)WDNNSSEQG;
 18 PAFSPAFDNL(pY)YWDNNSSEQG; PAFSPAFDNL(pY)(pY)WDNNSSEQG;
 19 PAFSPAFDNLY(pY)WDDNSSEQG; PAFSPAFDNL(pY)YWDDNSSEQG;
 20 PAFSPAFDNL(pY)(pY)WDDNSSEQG; PAFSPAFDNLY(pY)WDQASSEQG;
 21 PAFSPAFDNL(pY)YWDQASSEQG; PAFSPAFDNL(pY)(pY)WDQASSEQG;
 22 PAFSPAFDNLY(pY)WDQNASEQG; PAFSPAFDNL(pY)YWDQNASEQG; and
 23 PAFSPAFDNL(pY)(pY)WDQNASEQG.

1 7. The peptide as recited in claim 1, wherein at
 2 least one of X_1 and X_2 is an analog of phosphotyrosine, and
 3 said analog is (phosphonomethyl)phenylalanine.

1 8. A substantially pure peptide which is capable
 2 of binding a PTB domain, wherein the peptide is from 21 to
 3 about 100 amino acids in length and which comprises a core
 4 sequence of amino acids selected from the group consisting of
 5 AFGGAVENPE(pY)LAPRAGTASQ and EGTPTAENPE(pY)LGLDVPV.

1 9. A composition comprising a peptide as recited
 2 in claim 1, and a pharmaceutically acceptable carrier.

1 10. A method of determining whether a protein
 2 comprises a PTB domain, comprising the steps of:

3 contacting the protein with a peptide, which peptide
4 is from 5 to 100 amino acids in length and comprises a core
5 sequence of amino acids $NX_3X_1X_2X_4$, wherein X_1 is selected from
6 the group consisting of Y, pY, E, T, D, Q, A and F; X_2 is
7 selected from pY and Y, provided that at least one of X_1 and
8 X_2 is pY; X_3 is selected from the group consisting of L and A;
9 and X_4 is selected from the group consisting of W, L, S, F and
10 Q; and

11 determining whether the peptide binds to the protein
12 during said contacting step, where the binding of the peptide
13 to the protein is indicative that the protein comprises a PTB
14 domain.

1 11. The method as recited in claim 10, wherein
2 prior to said contacting step, the protein is attached to a
3 solid support;

4 the peptide used in said contacting step further
5 comprises a detectable group fused to the peptide; and

6 said determining step comprises assaying for the
7 presence of the detectable group.

1 12. The method as recited in claim 10, wherein
2 prior to said contacting step, the peptide is attached to a
3 solid support.

1 13. A method of determining whether a test compound
2 is an agonist or antagonist of a PTB/phosphorylated ligand
3 interaction, comprising the steps of:

4 incubating the test compound with a protein
5 comprising a PTB domain and a peptide, which peptide is from 5
6 to 100 amino acids in length and which comprises a core amino
7 acid sequence $NX_3X_1X_2X_4$, wherein X_1 is selected from the group
8 consisting of Y, pY, E, T, D, Q, A and F; X_2 is selected from
9 pY and Y, provided that at least one of X_1 and X_2 is pY; X_3 is
10 selected from the group consisting of L and A; and X_4 is
11 selected from the group consisting of W, L, S, F and Q; and

12 determining the amount of protein bound to the
13 peptide during said incubating step; and

14 comparing the amount of protein bound to the peptide
15 during said incubating step to an amount of protein bound to
16 the peptide in the absence of the test compound, the increase
17 or decrease in the amount of protein bound to the peptide in
18 the presence of the test compound being indicative that the
19 test compound is an agonist or antagonist of PTB
20 domain/phosphorylated ligand interaction, respectively.

1 14. A method of inhibiting the binding of a PTB
2 domain-containing protein to a tyrosine phosphorylated target,
3 comprising contacting the PTB domain-containing protein with
4 an effective amount of the peptide of claim 1.

1 15. The method as recited in claim 14, wherein the
2 tyrosine phosphorylated target is c-erbB2.

1 16. The method as recited claim 15, wherein the PTB
2 domain-containing protein is SHC.

1 17. A method of obtaining substantially pure PTB-
2 domain-containing protein from a mixture of different
3 proteins, comprising the steps of:

4 providing a peptide which is from 5 to 100 amino
5 acids in length, and which comprises a core amino acid
6 sequence $NX_3X_1X_2X_4$, wherein X_1 is selected from the group
7 consisting of Y, pY, E, T, D, Q, A and F; X_2 is selected from
8 pY and Y, provided that at least one of X_1 and X_2 is pY; X_3 is
9 selected from the group consisting of L and A; and X_4 is
10 selected from the group consisting of W, L, S, F and Q; bound
11 to a solid support;

12 contacting the mixture of different proteins with
13 the peptide bound to the solid support whereby the PTB domain-
14 containing protein is bound to the peptide;

15 washing the solid support to remove unbound
16 proteins; and

17 eluting substantially pure PTB-domain-containing
18 protein from the solid support.

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